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Title:
Perfect score:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    1127
852
849
754.5
684
590.5
574.5
525
520
521
520
512.5
463
440
373.8
                                                                                                                                                                                     Score
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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Gapop 10.0 -, Gapext 0.5
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1436
1 MKQILHPALETTAMTLFPVL.....KHQLVRDSCKASCNCSNSIX 258
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    GenCore version 5.1.3 Compugen Ltd
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sp_bacteria:*
sp_fungi:*
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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    09H108
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09NSD3
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3 08UW11
0 08UW25
0 08UW11
1 09R0V8
090XD3
090XE5
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090XE5
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O9h108 homo sapien
O88205 rattus norv
O99114 rattus norv
O99114 rottus cobal
O77720 equus cabal
O900259 mus musculu
O77719 equus cabal
O77719 extus bar
O8uw21 lapemis har
O8uw21 lapemis har
O90045 xenopus lae
O97818 sus scrofa
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4 4 4 4 5 4 3 2	38 39 40	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		17 18 19 20 21 22 23
252.5 252.5 249 248.5	274.5 274.5 263 258.5 256.5	285.5 280.5 279.5 278 278	291 291 288.5 288.5 288.5	344 311.5 311.5 308.5 295.5
17.8 17.6 17.3 17.3		19.5 19.5 19.4 19.3	20.3 20.3 20.1 20.1	24.0 22.8 21.7 21.7 21.5 20.6
253 207 208 415	424 100 425 332 301	523 434 188 424	258 415 258 380 392 500	255 489 489 236 236 371
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Q9H3Y0 Q20603 Q9N5N3 Q9N5N3	Q9XZ41 Q9DZT2 Q77153 Q9CQ35 Q9CQ35	Q98ST5 Q9BST5 Q9D2R3 Q99MM6 Q920U6 Q976744	Q99MM7 Q8TCB8 Q8TCB8 Q43692 Q9VFY2 Q9VFY2 Q906QR5 Q9H336	Q9CWG1 Q969K2 Q9JJ56 Q9JJ56 Q9ET66 Q9ET66 Q9AG6 Q96K61 Q96K61
Q9h3y0 homo sapien Q20603 caenorhabdi Q9n5n3 caenorhabdi Q44228 halocynthia	Q9xz41 ancylostoma Q9d2t2 mus musculu Q77153 ancylostoma Q9cq35 mus musculu Q95qf6 caenorhabdi	O98st5 gallus gall O98st5 gallus gall O9d2r3 mus musculu O99mm6 mus musculu O920u6 rattus norv O76744 necator ame	יַר בייַר בּ	Q9cwgl mus musculu Q969k2 homo sapien Q91j56 mus musculu Q9et66 mus musculu Q9da96 mus musculu Q9d106 homo sapien Q9fk61 homo sapien Q9fk08 homo sapien

ALIGNMENTS

Qy	Дb	Qy	Qu Be Ma	SQ	FΤ	DR	DR	DR	DR	DR	DR	DR	DR	DR	RL	RA	RP	RN	o ×	8	ጸ	SO	GN	DE	DE	DŢ	DT.	DŢ.	Å	ID	Q9H108	RESHLT
74 IKMEWNKEAAANAQKWANQCNYRHSNPKDRWTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133		14 MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNM 73	Query Match 78.5%; Score 1127; DB 4; Length 203; Best Local Similarity 99.5%; Pred. No. 1.8e-101; Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	SEQUENCE 203 AA; 22912 MW; F80D707EE0D81A2B CRC64;		PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.	E; PS01009; SCP_AG5_PR1_SC7_1;	SM00198; SCP; 1.	ProDom; PD000542; Allrgn_V5/Tpx1; 1.	PRINTS: PRO0837: V5TPXLIKE.	Pfam; PF00188; SCP; 1.		HSSP; P04284; 1CFE.	EMBL; AL121974; CAC19654.1;	Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.	Phillimore B.;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	DJ417L20.1.	(Fragment).	(Cysteine-rich se	(TrEMBLrel. 21, Last	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	-2001 (TrEMBLrel.	09H108;	Q9H108 PRELIMINARY; PRT; 203 AA.	08	

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RESULT
Q9R1L4
ID Q9
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DT 01
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X MEDLINE-9340864; PubMed-9675100;

A Maeda T., Sakashita M., Obba Y., Nakanishi Y.;

A Maeda T., Sakashita M., Obba Y., Nakanishi Y.;

T "Molecular cloning of the rat Tpx-1 responsible for the ir

between spermatogenic and sericli cells.";

L Blochem. Biophys. Res. Commun. 248:140-146(1998).

EMBL; AB009662; BAA32029.1; -.

R HSSP; P04284; ICFE.

R InterPro; IFR001283; Allrgn_V5/Tpx1.

R Ffam; PF00108; SCP; 1.

R FFAm; PF000842; Allrgn_V5/Tpx1; 1.

R PFADSTITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

R PROSTITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
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Best Local
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           Q9R1L4
Q9R1L4;
Q1-MAY-2000
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01-NOV-1998 (TREMBLrel. 08, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
Testis specific protein.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
             (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                             PRELIMINARY;
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             Created)
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Pred. No. 1.1e-74;
1; Mismatches 61;
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                                                             PRT;
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R EMBL; AFO78552; AADA48090.1,

R HSSP; P04284; 1CFE.

> R Interpro; IPR001283; Allrgn_V5/Tpx1.

> Pfam; PF00188; SCP; 1.

> PF PRINTS; PR00837; V5TPXLIKE.

DR PRODOM; PD000542; AALIGN_V5/Tpx1; 1.

DR SMART; SM00198; SCP; 1.

DR SMART; SM00198; SCP; 1.

DR PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_0; 1.

DR PROSITE; PS01010; SCP_AG5_PR1_SC7_0; 1.
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Best Local Similarity 61.2
Matches 150; Conservative
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01-DEC-2001 (
01-JUN-2002 (
Similar to ac
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STRAINSPRAQUE-DAWLEY;
STRAINE-98284327; PubMed=9621307;
O'BEYAN M.K., Loveland K.L., Herszfeld D., McFarlane J.R.,
de Kretser D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cysteine-rich secretory protein-2 crisp-2.
Strausberg R.; Strausberg R.; to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC011150; AAH11150.1; MGD; MGI:102553; Aeg1.
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                       TISSUE-SALIVARY GLAND;
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                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254
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.. Reprod. Dev. 50:313-322(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKMEWNKEAAANAQKWANQCNYRHSNPKDRWTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133
                                                                                                                                                                                                                                                                                                     1 (TERMBLrel. 19, Created)
1 (TERMBLrel. 19, Last sequence update)
2 (TERMBLrel. 21, Last annotation updatacidic epididymal glycoprotein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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; Pred. No. 2.2e-74;
31; Mismatches 62;
                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                      244 AA
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Best Local
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pfam; pP00188; SCP; 1.
probom; pD000542; Allrgn_V5/Tpx1; 1.
prosite; pS01009; SCP_AG5_pR1_SC7_1; UNKNOWN_1.
prosite; pS01010; SCP_AG5_pR1_SC7_2; UNKNOWN_1.
prosite; pS01010; SCP_AG5_pR1_SC7_2; UNKNOWN_1.
SEQUENCE 244 AA; 27622 MW; BDE122E22E5E8146
                                                                                                                                                                                                                                                                                       NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schambony A., Toepfer Petersen Submitted (JUN-1998) to the EMB EMBL; AJ006632; CAA07160.1; -HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cysteine-rich secretory protein-2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 077720
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO01283; Allrgn_V5/Tpx1.
Pfam; PP00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
Probom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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                        129 WFDEYNDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYYVCQYCPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNM 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
61
                                                                                                                     69 PARNMLKMEWNKEAAANAQKWANQCNYRHSNPKDRMTSLKCGENLYMSSAPSSWSQAIQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGKIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDLTYDVGPKQPDSVVGHYTQVVWNSTFQVACGVAECP-KNPLRYYYVCHYCPVGNYQGR 179
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HYDESLDFTYGVGPKSAGSVVGHYTQAVWYSSYRVGCGIAYCPNQESLKYYYVCQYCPVG
                                                                                             PASNMLKMEWSREATANAKRWANKCTLEHSSADDRKTSTRCGENIYMSSDPTPWSDAIQS
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165 AA;
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                                                                                                                                                                                                                                                                                         165
18402 MW;
                                                                                                                                                                                                                47.68;
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54.3%; Pred. No. 3.3
Live 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ
                                                                                                                                                                                            18;
                                                                                                                                                                                          Score 684; DB 6; I
Pred. No. 1.4e-58;
8; Mismatches 32;
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                                                                                                                                                                                                                                                                                            91172E8A7D4680B9 CRC64;
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72;
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                                                                                                                                                                                                                                        Length 165;
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Best Local
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EPIDIDYMIS;
MEDLINE-21085660; PubMed-11217851;
MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii }
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gentzel M., Schambony A., Toepfer-Petersen E.;
"Identification of GRISP proteins of staliton'
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ (
EMBL; AJ277708; CAB90614.1;
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam, PF00188; SCp; 1.
PRINTS; PR00837; V5TPXLIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
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01-OCT-2000 (TREMBLrel. 15, Last sequence update)
01-UN-2002 (TREMBLrel. 21, Last annotation update)
Cysteine-rich secretory protein-2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9N0J2
                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                               9230112K08RIK protein.
9230112K08RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 LKMEWNKEAAANAQKWANQCNYRHSNPKDRMTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WAANRIYUPYEQGAPCASCEDNCDDGLCTNGCKYEDLYSNCKELK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDFTYGVGPKSAGSVVGHYTQAVWYSSFRVGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKMEWSREATANAQKWANKCTLEHSSADDRKTSTRCGENIYMSSDPTPWSDAIQSWYDES 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO0837; V5TPXLIKE.
PD000542; Allrgn_V5/Tpx1;
SM00198; SCP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AA;
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                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16703 MW;
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17,
21,
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Pred. No. 1.5e
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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databases.
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                                                                                                                                                                                                                                                                            Murinae;
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Best Local S
Matches 113
                                                                                                                                                                                                                                                                                                                                     O9XSD3;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Androgen-dependent acidic epididymal glycoprotein.
Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gassterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Washiwa-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Lawashi J., Washirayi Y.
O'Rand M.G.;

"Cloning and characterization of an androgen dependent acidic epididymal glycoprotein/crisp1-like protein from the monkey.",

J. Androl. 20:0-0(1999).

EMBL; AF123894; AAD27611.1; -

EMBL; AF123894; AAD27611.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00837; V5TPXLIKE.
Probom; PD000542; Alityn_V5/TpX1; 1.
SMART; SM0198; SCP; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
SEQUENCE 250 AA; 28704 MW; 747B45FF2FBDB9D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK020340; BAB32077.1; -.
MGD; MGI:1925331; 9230112K08Rik.
InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                            SEQUENCE FROM N.A.
Sivashanmugam P., Richardson R.T., Hall S., Hamil K.G., French F.S.,
                                                                                                                                                                                                                                                                                         Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9XSD3
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Pred. No. le
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                                                                                                         from the monkey.";
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Best Local S
Matches 98
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Best Local S
Matches 109
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ProDom; PD000542; Alirgn_V5/Tpx1; 1.

SMART; SM00198; SCF; 1.

PROSITE; PS01010; SCF_AG5_PR1_SC7_2; 1.

PROSITE; PS01010; SCF_AG5_PR1_SC7_2; 1.
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                                                                                                                                                                                                                                                                              PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PS071010; SCP_AG5_PR1_SC7_2; NON_TER 1 1 1 1 86AA67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TERMBLrel. 08, Created)
01-NOV-1998 (TERMBLrel. 08, Last sequence update)
01-UN-2002 (TERMBLrel. 21, Last annotation updat
Cysteine-rich secretory protein-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
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Schambony A., Toepfeer-Petersen E.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
EMBL; AJ006631; CAA07159.1; -
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
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                                                                   YVPYEQGAPCASCPDNCDDGLCTNGCKYEDLYSNCKSLKLTLTCKHQLVRDSCKASCNCS
RMTSLKCGENLYMSSAPSSWSQAIQSWFDEYNDFDFGVGPKTPN-AVVGHYTQVVWYSSY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEPYKKGVPCEACPNNCEDKLCTNPCIYYDEYTDCSLEVRFLGCNHSTPRMFCKATCLCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDFGVGPKTPNAV-VGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYYVCQYCPAGNWANRL 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EWNKEAAANAQKWANQCNYRHSNPKD-RWTSLKCGENLYMSSAPSSWSQAIQSWFDEYND 135
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44.9%; Pred. No. 1.3e-44;
vative 34; Mismatches 95;
                                                                                                                                                                                                36.6%;
                                                                                                                                                                        33;
                                                                                                                                                                        Score 525; DB 6;
Pred. No. 5.5e-43;
3; Mismatches 83
                                                                                                                                                                                                                                                                                 86AA6778A244CAE8 CRC64;
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RESULT CONTROL OF CONT
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A novel cysteine rich venom protein cDNA from sea snake.";

L Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF199861: AAL54918.1; -.

R InterPro; IPR001283; AAl1rgn_V5/Tpx1.

R PFAm; PF00188; SCP; 1.

R PFAm; PF00189; SCP; 1.

R PRINTS; PR00837; V5TPXLIKE.

R PRINTS; PR00837; V5TPXLIKE.

R PROSITE; PS010109; SCP, AG5_PR1_SC7_1; UNKNOWN_1.

R PROSITE; PS011019; SCP_AG5_PR1_SC7_2; UNKNOWN_1.

R PROSITE; PS011019; SCP_AG5_PR1_SC7_2; UNKNOWN_1.

R PROSITE; PS011019; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cystelne-rich venom protein.
Lapemis hardwicki (Hardwick's sea snake).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Hydrophiinae; Lapemis.
                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cystaine-rich venom protein.
Lapemis hardwickii (Hardwick's sea snake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
RCBL_TaxID-8781;
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46.4%; Pred. No. 1.3e-42;
tive 35; Mismatches 59)
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Best Local S
Matches 96
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*A Novel Cysteine-Rolch Venom Protein Precursor (CRVP) mRNA fro
T Snake (Lapemis Hardwicki).*;

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF15541; AAL54896.1: -.

R InterPro; IPR001283; Allrgn_V5/Tpx1.

R Pfam; PF00188; SCP; 1.

R PRINTS; PR00837; V5TPXLIKE.

R PRODOMS; DP000542; Allrgn_V5/Tpx1: 1.

R SNART; SM00198; SCP; 1.

R PROSITE: PS01009; SCP_AG5_PR1_SC7_1; UNKNOWN_1.

R PROSITE: PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.

R PROSITE: PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.

R PROSITE: PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
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Best Local
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PROSITE;
PROSITE;
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Gentzel M., Schambony A., Toepfer-Petersen E.;
"Identification of CRISP proteins of stallion and bull.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ277709; CAB90615.1; -.
HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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                 148
                                                                                                                                                                                                            Pfam; PF00188; SCP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YNDFDFGYGPKTPNAVYGHYTQVVWYSSYLYGCGNAYCPNQKYLKYYYYCQYCPAGNWAN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLYVPYEQGAPCASCPDNCDDGLCTN 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOMKWNSRAAQNAKRSADRCTFAHSPEHTRTVGKFRCGENIFMSSOPFAWSGVVODWYDE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 46.6
96; Conservative
                                             1 Similarity
77; Conserv
                                                                                                                                             PR00837; V5PPXLIKE.

PD000542; Allrgn_V5/Tpx1; 1.

;; PS01009; SCP_AG5_PR1_SC7_1;

;; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                             IPR001283; Allrgn_V5/Tpx1.
)188; SCP; 1.
                                                                                                     111
111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
ch secretory protein-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.7%; Score 512.5; DB 13; Length 199;
46.6%; Pred. No. 8e-42;
vative 35; Mismatches 66; Indels 9;
12284 MW; B5438EA103C0B941 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                          32.2%;
                                             12;
                                          Score 463; DB 6; I
Pred. No. 2.5e-37;
2; Mismatches 22;
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                                                                         Length 111;
                                             Indels
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                                             Gaps
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                 207
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.2e-28; les 63;

Indels Length

7;

Gaps

5

DB 4;

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RESULT
Q96SF6
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ROCCORDITA
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Best Local
                                                                                  Q96SF6 PRELIMINARY; PRT
Q96SF6; PRELIMINARY; PRT
Q96SF6; Control (TremBLrel 19, Creat)
01-DEC-2001 (TremBLrel 19, Last;
01-JUN-2002 (TremBLrel 21, Last;
BA719J20.1.2 (acidic epididymal g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9R0V8
Q9R0V8;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Acidic epididymal glycoprotein D/E (Fragment).
CRISP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY;
Klemme L.M., Siteri J.E., Hamilton D.W.;
The Rat Androgen-Regulated Acidic Epididymal Protein D (rCrisp-1)
Gene: Structural Comparison with Other Crisp Genes, Identification
Alternative Transcripts and of Transcriptional Regulatory Elements.
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpxl; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U60956; AAD41529.1; --
EMBL; U60953; AAD41529.1; JOINED.
EMBL; U60954; AAD41529.1; JOINED.
EMBL; U60955; AAD41529.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00188; SCP;
                                                                                                                                                                                                                                            208
                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                          74 LKMEWNKEAAANAQKWANQCNYRHSNPKDRWTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                 16 LFPVLLFLVAGLLPSF--PANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNM 73
                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                         LRVEWDHDAYVNAQKWANRCIYNHSPLQHRTTTLKCGENLFMANYPASWSSVIQDWYDES
                                                                                                                                                                                                                                                                                                                                                                    LMLVLLFLAAVLPPSLLQDTTDEWDRDLENLSTTKLSVQEEIINKHNQLRRTVSPSGSDL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGDCDDGLCTNTCQYEDLLSNCDSLKKTAGCGHELLKEKCKATCLCEGKIY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDNCDDGLCTNGCKYEDLYSNCKSLKLTLTCKHQLVRDSCKASCNCSNSIY 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVGHYTQVVWYSSYRVGCGIAYCPNQENLKYYYVCQYCPAGNNVSKKNTPYKEGTPCASC
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS01009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 158
158 AA; 17975 MW; 26E53DAB08798EA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCP_AG5_PR1_SC7_1;
                                                                                                                                                                                                                                                                                                                                                                                                                             30.6%; Score 440; DB 54.1%; Pred. No. 6.6e tive 21; Mismatches
                                                                                    Last sequence update)
Last annotation update)
ymal glycoprotein-like 1
                                                                                                                                     Created)
                                                                                                                                                                    178
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6.6e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 158;
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Best Local S
Matches 69
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Best Local
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SEQUENCE
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Williams S.;

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AL359458; CAC34981.1; -

InterPro; IPR001283; Allrgn_V5/Tpx1.

Pfam; PF00188; SCP; 1.

ProDom; PD000542; Allrgn_V5/Tpx1; 1.

PROSITE; PS01009; SCP_AC5_PR1_SC7_1; UNKNOWN_1.

SEQUENCE 178 AA; 20462 MW; 18739B2B6EBF7F84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-21457293; PubMed-11562501;
Olson J.H., Xiang X., Ziegert T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allurin (Fragment).

Xenopus laevis (African clawed frog).

Zenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                    Prodom; PD000542; Allrgn_V5/Tpx1; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; UNKNOWN_1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                  related to mammalian sperm-binding proteins.";
Proc. Natl. Acad. Sci. U.S.A. 98:11205-11210(2001).
EMBL; AF393653; AAL12003.1;
InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q90XE5
                                                                                                                                                                                                                                                                                                                                      Pfam; PF00188; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                     "Allurin, a 21-kDa sperm chemoattractant from Xenopus related to mammalian sperm-binding proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                Chandler D.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q90XE5;
            119
                                         188
                                                                                                    128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 SFKHGEWTTTDDDITTDHYTQIVWATSYLIGCAIASCRQQGSPRYLYVCHYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 DFDFGVGPKTPNAV-VGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYYVCQYC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 MEWNKEAAANAQKWANQCNYRHSNPKD-RWTSLKCGENLYMSSAPSSWSQAIQSWFDEYN 134
                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 LLFLVAG--LLP--SFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNMLK 75
                                                                                                                                                               72 NMLKMEWNKEAAANAQKWANQCNYRHSNPKDR----MTSLKCGENLYMSSAPSSWSQAIQ 127
                                                                                                                                 1 DMKKMVWCDPAALNAYNFATQCSMYHSLVEERHIKEPIDVVCGENIYMSTAKSDWSTVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LLFLVAAACLLPMLSMKKKSARD-QFNKLVTDLPNVQEEIVNIHNALRRVVPPASNMLK 64
                               GNWANRLYVPYEQGAPCASCPDNCDDGLC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSWSEEAAQNARIFSKYCDMTESNPLERRLPNTFCGENMHMTSYPVSWSSVIGVWYSEST
            GNMDESVPRPYEEGEWCASCPESCODKLC
                                                                      SWYNERSDFAYGKG-KISDKPIGHYTQVVWAKSYLLGCAYNFCKENK-YPHVFVCHYGPM
                                                                                                      SWFDEYNDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPNQKVEKYYYVCQYCPA 187
                                                                                                                                                                                               69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                          153 AA; 17684 MW; E01A246785FC36CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                            24.9%; Score 358; DB 13;
46.3%; Pred. No. 5.8e-27;
vative 22; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ziegert T., Kittelson A., Rawls A., Bieber A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 373.5; I
Pred. No. 2.2e
21; Mismatches
            147
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ξ

176

Length 153;

egg

Indels

6;

Gaps

w

60

Search completed: March 14, 2003, 05:42:59 Job time: 52.2472 secs